

RAW SEQUENCE LISTING DATE: 12/06/2000
 PATENT APPLICATION: US/09/499,526 TIME: 13:17:01

Input Set : A:\Pto.amc
 Output Set: N:\CRF3\12062000\I499526.raw

SEQUENCE LISTING

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2 (1) GENERAL INFORMATION:
3   (i) APPLICANT: Lu, Kuang-hui
4             Pang, Kevin
5   (ii) TITLE OF INVENTION: Methods and Reagents for Treating
6             Glucose Metabolic Disorders
7   (iii) NUMBER OF SEQUENCES: 3
9   (iv) CORRESPONDENCE ADDRESS:
10      (A) ADDRESSEE: Foley, Hoag & Eliot
11      (B) STREET: One Post Office Square
12      (C) CITY: Boston
13      (D) STATE: MA
14      (E) COUNTRY: USA
15      (F) ZIP: 02109
16   (v) COMPUTER READABLE FORM:
17      (A) MEDIUM TYPE: Floppy disk
18      (B) COMPUTER: IBM PC compatible
19      (C) OPERATING SYSTEM: PC-DOS/MS-DOS
20      (D) SOFTWARE: ASCII (text)
21   (vi) CURRENT APPLICATION DATA:
C--> 22      (A) APPLICATION NUMBER: US/09/499,526
C--> 23      (B) FILING DATE: 10-Feb-2000
24      (C) CLASSIFICATION:
25   (vii) ATTORNEY/AGENT INFORMATION:
26      (A) NAME: Vincent, Matthew P.
27      (B) REGISTRATION NUMBER: 36,709
28      (C) REFERENCE/DOCKET NUMBER: ONV-058.01
29   (ix) TELECOMMUNICATION INFORMATION:
30      (A) TELEPHONE: (617) 832-1000
31      (B) TELEFAX: (617) 832-7000
32 (2) INFORMATION FOR SEQ ID NO: 1:
33   (i) SEQUENCE CHARACTERISTICS:
34      (A) LENGTH: 36 amino acids
35      (B) TYPE: amino acid
36      (D) TOPOLOGY: linear
37   (ii) MOLECULE TYPE: protein
38   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
39   Tyr Pro Ile Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu
40   1      5      10      15
41   Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr
42      20      25      30
43   Arg Gln Arg Tyr
44      35
C--> 47 (2) INFORMATION FOR SEQ ID NO: 2:
48   (i) SEQUENCE CHARACTERISTICS:
49      (A) LENGTH: 582 base pairs
50      (B) TYPE: nucleic acid

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51          (C) STRANDEDNESS: not relevant
W--> 52          (D) TOPOLOGY: not relevant
53          (ii) MOLECULE TYPE: cDNA
54          (ix) FEATURE:
55              (A) NAME/KEY: CDS
56              (B) LOCATION: 81..371
57          (ix) FEATURE:
58              (A) NAME/KEY: sig_peptide
59              (B) LOCATION: 81..164
60          (ix) FEATURE:
61              (A) NAME/KEY: mat_peptide
62              (B) LOCATION: 165..371
63          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
64 CAGCITGACC TCGGGCAGTG CAGCCCTTGG GACTTCCCTC GCCTTCCACC TCCTGCTCGT      60
65 CTGCTTCACA AGCTATCGCT ATG GTG TTC GTG CGC AGG CCG TGG CCC GCC      110
66          Met Val Phe Val Arg Arg Pro Trp Pro Ala
67          -28      -25      -20
68 TTG ACC ACA GTG CTT CTG GCC CTG CTC GTC TGC CTA GGG GCG CTG GTC      158
69 Leu Thr Thr Val Leu Leu Ala Leu Val Cys Leu Gly Ala Leu Val
70          -15      -10      -5
71 GAC GCC TAC CCC ATC AAA CCC GAG GCT CCC GGC GAA GAC GCC TCG CCG      206
72 Asp Ala Tyr Pro Ile Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro
73          1      5      10
74 GAG GAG CTG AAC CGC TAC TAC GCC TCC CTG CGC CAC TAC CTC AAC CTG      254
75 Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu
76 15      20      25      30
77 GTC ACC CGG CAG CGG TAT GGG AAA AGA GAC GGC CCG GAC AGG CTT CTT      302
78 Val Thr Arg Gln Arg Tyr Gly Lys Arg Asp Gly Pro Asp Arg Leu Leu
79          35      40      45
80 TCC AAA ACG TTC TTC CCC GAC GGC GAG GAC CGC CCC GTC AGG TCG CGG      350
81 Ser Lys Thr Phe Phe Pro Asp Gly Glu Asp Arg Pro Val Arg Ser Arg
82          50      55      60
83 TCG GAG GGC CCA GAC CTG TGG TGAGGACCCC TGAGGCCTCC TGGGAGATCT      401
84 Ser Glu Gly Pro Asp Leu Trp
85          65
86 GCCAACCAGG CCCACGTGAT TTGCATACGC ACTCCCGACC CCAGAAACCC GGATTCTGCC      461
87 TCCCGACGGC GCGGTCTGGG CAGGTTTCGG GTGCGGCCCT CCGCCCGCGT CTCGGTGCCC      521
88 CCGCCCCCTG GCGTGGAGGG CTGTGTGTGG TCCTTCCCTG GTCCCAAAT AAAGAGCAAA      581
89 T      582
C--> 90 (2) INFORMATION FOR SEQ ID NO: 3:
91          (i) SEQUENCE CHARACTERISTICS:
92              (A) LENGTH: 97 amino acids
93              (B) TYPE: amino acid
94              (D) TOPOLOGY: linear
95          (ii) MOLECULE TYPE: protein
96          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
97 Met Val Phe Val Arg Arg Pro Trp Pro Ala Leu Thr Thr Val Leu Leu
98 -28      -25      -20      -15
99 Ala Leu Leu Val Cys Leu Gly Ala Leu Val Asp Ala Tyr Pro Ile Lys

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DEC 11 2000

TECH CENTER 1600/2900

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100		-10				-5						1				
101	Pro	Glu	Ala	Pro	Gly	Glu	Asp	Ala	Ser	Pro	Glu	Glu	Leu	Asn	Arg	Tyr
102		5				10					15					20
103	Tyr	Ala	Ser	Leu	Arg	His	Tyr	Leu	Asn	Leu	Val	Thr	Arg	Gln	Arg	Tyr
104					25						30					35
105	Gly	Lys	Arg	Asp	Gly	Pro	Asp	Arg	Leu	Leu	Ser	Lys	Thr	Phe	Phe	Pro
106				40						45						50
107	Asp	Gly	Glu	Asp	Arg	Pro	Val	Arg	Ser	Arg	Ser	Glu	Gly	Pro	Asp	Leu
108				55						60						65
109	Trp															

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DEC 11 2000

TECH CENTER 1600/2500

VERIFICATION SUMMARY DATE: 12/06/2000
PATENT APPLICATION: US/09/499,526 TIME: 13:17:02

Input Set : A:\Pto.amc
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L:22 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:23 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:47 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]
L:52 M:246 W: Invalid value of Alpha Sequence Header Field, {TOPOLOGY:}, SeqNo=2, Value=[not relevant]
L:90 M:220 C: Keyword misspelled or invalid format, [(2) INFORMATION FOR SEQ ID NO:]